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In the claims:

Please amend the claims as follows:

Claims 1 to 5 are withdrawn.

6. (currently amended) A method of providing an array of proteins, the method comprising:

providing a substrate with a plurality of addresses; and

providing at each address at least (i) a nucleic acid encoding an amino acid sequence comprising a test amino acid sequence and an affinity tag, and (ii) a binding agent that recognizes the affinity tag.

7. (currently amended) A method of providing an array of proteins, the method comprising:

providing a substrate with a plurality of addresses, each address comprising (i) a nucleic acid encoding an a hybrid amino acid sequence comprising a test amino acid sequence and an affinity tag, and (ii) a binding agent that recognizes the affinity tag;

contacting each address of the plurality with a translation effector to thereby translate the hybrid amino acid sequence; and

maintaining the substrate under conditions permissive for the <u>hybrid</u> amino acid sequence to bind the binding agent.

Claims 8 and 9 are withdrawn.

10. (currently amended) A method of producing a protein interaction map for a plurality of amino acid sequences, the method comprising:

providing (i) a first plurality of nucleic acids, each encoding an amino acid sequence comprising an <u>a test</u> amino acid sequence of the plurality of amino acid sequences and an affinity tag; (ii) a second plurality of nucleic acids, each encoding an amino acid sequence comprising an <u>a test</u> amino acid sequence of the plurality of amino acid sequences and a recognition tag; and

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(iii) a substrate with a plurality of addresses and a binding agent that binds the affinity tag and is attached to the substrate; and

disposing on the substrate, at each address, a nucleic acid of the first plurality and a

nucleic acid of the second plurality;

— contacting each address of the plurality with a translation effector to thereby translate the hybrid amino acid sequence;

— maintaining the substrate under conditions permissive for the affinity tag to bind binding agent;

— washing the substrate to remove the translation extract and unbound polypeptides; and detecting the recognition tag at each of the plurality of addresses.

11. (currently amended) A method comprising:

providing a substrate comprising a providing a substrate comprising a plurality of addresses, each address of the plurality having a binding agent;

providing a plurality of nucleic acid sequences, each nucleic acid sequence comprising a sequence encoding a test amino acid sequence and an affinity tag that is recognized by the binding agent;

providing on a server a list of either (i) nucleic acid sequences of the plurality or (ii) subsets of the plurality;

transmitting, from a server, one or more choices for amino acids to include on the substrate the list across a network to a user;

receiving at least one selection of the list from the user; and

disposing the one or more nucleic acid sequence corresponding to the selection on an address of the plurality; and

providing the substrate to the user.

12. (new) The method of claim 6 further comprising contacting each address of the plurality with a transcription effector.

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13. (new) The method of claim 6 further comprising contacting each address of the plurality with a translation effector.

- 14. (new) The method of claim 6 further comprising contacting each address of the plurality with a transcription effector and a translation effector.
- 15. (new) The method of claim 13 wherein the translation effector comprises a translation extract prepared from cells.
- 16. (new) The method of claim 13 further comprising contacting each address of the plurality with a chaperone.
- 17. (new) The method of claim 6 further comprising enclosing the substrate in an air- or water- resistant package.
 - 18. (new) The method of claim 6 wherein each test amino acid sequence is unique.
- 19. (new) The method of claim 6 wherein the affinity tag is separated from the test amino acid sequence by at least five amino acids.
- 20. (new) The method of claim 6 wherein the affinity tag encoded by the nucleic acid at each address of the plurality is the same.
- 21. (new) The method of claim 6 wherein the affinity tag encoded by the nucleic acid at an address of the plurality differs from at least one other affinity tag in the plurality of addresses.
 - 22. (new) The method of claim 6 wherein the nucleic acid is DNA.
 - 23. (new) The method of claim 22 wherein the nucleic acid is double stranded DNA.

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24. (new) The method of claim 22 wherein the nucleic acid comprises an operably linked transcription promoter.

- 25. (new) The method of claim 6 wherein the nucleic acid comprises an internal ribosome entry site.
- 26. (new) The method of claim 6 wherein the nucleic acid comprises a plurality of cistrons.
- 27. (new) The method of claim 6 wherein the nucleic acid comprises a sequence that encodes a reporter protein.
- 28. (new) The method of claim 27 wherein the reporter protein can produce or modulate light.
- 29. (new) The method of claim 6 wherein the transcription promoter is a prokaryotic promoter.
 - 30. (new) The method of claim 6 wherein the amino acid sequence comprises an intein.
 - 31. (new) The method of claim 6 wherein the substrate is partitioned.
- 32. (new) The method of claim 6 wherein the substrate comprises at least 1 address per cm².
- 33. (new) The method of claim 32 wherein the substrate comprises at least 10 addresses per cm².
- 34. (new) The method of claim 6 wherein each address contains less than 1 ng of the nucleic acid.

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35. (new) The method of claim 6 wherein each address contains less than 10 pg of the nucleic acid.

- 36. (new) The method of claim 6 wherein the binding agent comprises a biological polymer.
- 37. (new) The method of claim 6 wherein the binding agent is covalently attached to the substrate.
- 38. (new) The method of claim 6 wherein the binding agent is attached by a bridging moiety.
 - 39. (new) The method of claim 6 wherein the binding agent is an antibody.
- 40. (new) The method of claim 6 wherein affinity tag comprises a polypeptide sequence which can chelate metal.
 - 41. (new) The method of claim 40 wherein affinity tag comprises hexa-histidine.
- 42. (new) The method of claim 6 wherein affinity tag comprises a protein selected from the group consisting of glutathione-S-transferase, chitin binding protein, cellulase, maltose binding protein, dihydrofolate reductase, and FK506 binding protein (FKBP).
- 43. (new) The method of claim 13 further comprising contacting each address of the plurality with a protein-modifying enzyme.
- 44. (new) The method of claim 6 wherein the nucleic acid comprises a site-specific recombination site.

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45. (new) The method of claim 6 wherein each address comprises a plurality of nucleic acid sequences, each encoding a unique test amino acid sequence and an affinity tag.

- 46. (new) The method of claim 6 wherein the providing comprises mechanically delivering the nucleic acid to each address of the plurality of addresses.
- 47. (new) The method of claim 6 wherein the providing comprises amplifying a template nucleic acid to provide a nucleic acid for each address of the plurality of addresses.
- 48. (new) The method of claim 7 further comprising contacting cells to the substrate and evaluating the cells or a parameter of the cells.
- 49. (new) The method of claim 7 further comprising contacting members of a display library to the substrate.
- 50. (new) The method of claim 7 further comprising contacting a patient sample to the substrate.
- 51. (new) The method of claim 50 further comprising further comprising detecting binding of the patient sample to the array.
- 52. (new) The method of claim 51 further comprising recording results of the detecting in a database.
- 53. (new) The method of claim 7 wherein the test amino acid sequences at the plurality of addresses comprise allergens and/or auto-immune antigens.
- 54. (new) The method of claim 7 wherein the test amino acid sequences at the plurality of addresses comprise naturally occurring sequences.

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55. (new) The method of claim 54 wherein the test amino acid sequences at the plurality of addresses comprise bacterial antigens.

- 56. (new) The method of claim 54 wherein the test amino acid sequences at the plurality of addresses comprise viral antigens.
- 57. (new) The method of claim 56 wherein the viral antigens comprise antigens from a rotavirus, hepatitis virus, herpes virus, papilloma virus and/or a retrovirus.
- 58. (new) The method of claim 7 wherein the test amino acid sequences at the plurality of addresses comprise artificial amino acid sequences.
- 59. (new) The method of claim 7 wherein the test amino acid sequences at the plurality of addresses comprise transmembrane proteins whose transmembrane domains have been excised.
- 60. (new) The method of claim 7 wherein the test amino acid sequences at the plurality of addresses comprise randomized amino acid sequences.
- 61. (new) The method of claim 7 wherein the test amino acid sequence comprises an immunoglobulin variable domain.
- 62. (new) The method of claim 7 further comprising contacting endoplasmic reticulum vesicles to the array.
- 63. (new) The method of claim 7 wherein the substrate comprises at least 10 addresses per cm².
- 64. (new) The method of claim 7 wherein each address contains less than 1 ng of the nucleic acid.

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65. (new) The method of claim 7 wherein each address contains less than 10 pg of the nucleic acid.

- 66. (new) The method of claim 22 wherein the DNA comprises plasmid DNA.
- 67. (new) The method of claim 22 wherein the DNA comprises a PCR product.
- 68. (new) The method of claim 6 wherein the providing of nucleic acid at each address comprise:

providing a collection of nucleic acids, each member of the collection being compatible with a recombinational cloning system and including an open reading frame of interest;

recombining members of the collection with a recipient nucleic acid that comprises a nucleic acid sequence encoding an affinity tag such that the open reading frame is linked in frame to the nucleic acid sequence encoding the affinity tag; and

disposing nucleic acid derived from the recombination at addresses of the plurality of addresses.

- 69. (new) The method of claim 68 wherein the collection comprises at least 500 members.
- 70. (new) The method of claim 68 wherein members of the collection are identified by a locator accessible to a robotic system.
- 71. (new) The method of claim 68 wherein members of the collection are referenced by a relational database that includes information about storage location and a link to another biological database.

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72. (new) The method of claim 7 wherein each address further comprises a nucleic acid encoding a modifying enzyme.

- 73. (new) The method of claim 72 wherein the modifying enzyme is varied among the addresses of the plurality.
 - 74. (new) The method of claim 10 further comprising:

contacting each address of the plurality with a translation effector to thereby translate the nucleic acid of the first plurality and the nucleic acid of the second plurality; and

maintaining the substrate under conditions permissive for the affinity tag to bind the binding agent.

- 75. (new) The method of claim 74 further comprising washing the substrate to remove the translation extract and unbound polypeptides.
- 76. (new) The method of claim 75 further comprising detecting the recognition tag at addresses of the plurality of addresses.
- 77. (new) The method of claim 10 wherein the recognition tag comprises an epitope tag, an enzyme, or a fluorescent protein.
 - 78. (new) The method of claim 11 further comprising providing the substrate to the user.
- 79. (new) The method of claim 11 wherein the server is interfaced with a robotic system, and the at least one selection is communicated from the server to the robotic system.
 - 80. (new) The method of claim 11 wherein the choices are arranged hierarchically.
- 81. (new) The method of claim 11 wherein the choices comprise a list of general user needs.

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82. (new) The method of claim 11 wherein the choices comprise a list of classes of amino acid sequences.

- 83. (new) The method of claim 11 wherein the choices comprise individual amino acid sequences.
- 84. (new) The method of claim 82 wherein the classes comprise entries correlated with a condition or disease.
- 85. (new) The method of claim 82 wherein the classes comprise entries correlated with a protein family.
- 86. (new) The method of claim 82 wherein the classes comprise entries correlated with an organismal species.
- 87. (new) The method of claim 11 wherein the server recommends a control amino acid sequence based on user selections.
- 88. (new) The method of claim 7 further comprising evaluating the substrate for a fluorescence.
- 89. (new) The method of claim 7 further comprising evaluating the substrate using mass spectroscopy.
- 90. (new) The method of claim 7 further comprising evaluating the substrate for a fluorescent property.
- 91. (new) The method of claim 7 further comprising evaluating the substrate for an enzymatic property.

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92. (new) The method of claim 7 further comprising evaluating the plurality of addresses on the substrate, and recording results of the evaluating in records of a database.

- 93. (new) The method of claim 92 further comprising clustering the records to identify addresses which are related.
- 94. (new) The method of claim 92 further comprising making results of the evaluating accessible to a network of health care providers.
- 95. (new) The method of claim 92 further comprising making results of the evaluating accessible to a physician.